

SEQUENCE LISTING

<110> Helix Research Institute

<120> FATTY ACID TRANSPORTER PROTEINS AND THE GENES ENCODING THE PROTEINS

<130> H1-106DP3PCT

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<150> JP 1999-194179

<151> 1999-07-08

<150> JP 2000-128993

<151> 2000-04-25

<150> US 60/159586

<151> 1999-10-18

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<170> PatentIn Ver. 2.0

<210> 1

<211> 2405

<212> DNA

<213> Homo sapiens

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<221> CDS

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gcaactcctcc cgggtttctg ctctccgccc gtgtggagtg gtgggggcct ggggtggga 58

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Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln

1

5

10

15

cta gaa cga gcg gcc cta ggt ttt cgg aag gga gga tca ggg atg ttt 154
Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Ser Gly Met Phe
20 25 30gcg agc ggc tgg aac cag acg gtg ccg ata gag gaa gcg ggc tcc atg 202
Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
35 40 45

gct gcc ctc ctg ctg ccc ctg ctg ttg cta ccg ctg ctg ctg		250
Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Pro Leu Leu Leu		
50	55	60
ctg aag cta cac ctc tgg ccg cag ttg cgc tgg ctt ccg gcg gac ttg		298
Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu		
65	70	75
80		
gcc ttt gct gtc gca gtc tgg tgg aaa agg gct ctt cga gct cgc		346
Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg		
85	90	95
gcc ctg gcc gct gcc gac ccg gaa ggt ccc gag ggg ggc tgc		394
Ala Leu Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Cys		
100	105	110
agc ctg gcc tgg cgc ctc gct gaa ctg gcc cag cag cgc gcc gct cac		442
Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His		
115	120	125
acc ttt ctc att cac ggc tcg cgg cgc ttt agc tac tca gag gct gag		490
Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu		
130	135	140
cgc gag agt aac agg gct gca cgc gcc ttc cta cgt gct cta ggc tgg		538
Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp		
145	150	155
160		
gac tgg gga ccc gac ggc gac agc ggc gag ggg agc gct gga gaa		586
Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu		
165	170	175
ggc gag cgg gca gct ccg gga gcc gga gat gca gct gcc gga agc ggc		634
Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Gly Ser Gly		
180	185	190
gct gag ttt gcc gga ggg gac ggt gcc gcc aga ggt gga gga gct gcc		682
Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Ala Ala		
195	200	205
gcc cct ctg tca cct gga gca act gtg gct ctc ctc ccc gct ggc		730
Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly		
210	215	220
cca gag ttt ctg tgg ctc tgg ttc ggg ctg gcc aag gct ggc ctc cgc		778
Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg		

225	230	235	240	
act gcc ttt gtg ccc acc gcc ctg cgc cg ^g ggc ccc ctg ctg cac tgc Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys				826
245	250	255		
ctc cgc agc tgc ggc gcg cgc g ^c ctg gtg ctg g ^c cca gag ttt ctg Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu				874
260	265	270		
gag tcc ctg gag ccg gac ctg ccc gcc ctg aga gcc atg ggg ctc cac Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His				922
275	280	285		
ctg tgg gct gca ggc cca gga acc cac cct gct gga att agc gat ttg Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu				970
290	295	300		
ctg gct gaa gtg tcc gct gaa gtg gat ggg cca gtg cca gga tac ctc Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu				1018
305	310	315	320	
tct tcc ccc cag agc ata aca gac acg tgc ctg tac atc ttc acc tct Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser				1066
325	330	335		
ggc acc acg ggc ctc ccc aag gct gct cgg atc agt cat ctg aag atc Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile				1114
340	345	350		
ctg caa tgc cag ggc ttc tat cag ctg tgt ggt gtc cac cag gaa gat Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp				1162
355	360	365		
gtg atc tac ctc gcc ctc cca ctc tac cac atg tcc ggt tcc ctg ctg Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu				1210
370	375	380		
ggc atc gtg ggc tgc atg ggc att ggg gcc aca gtg gtg ctg aaa tcc Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser				1258
385	390	395	400	
aag ttc tcg gct ggt cag ttc tgg gaa gat tgc cag cag cac agg gtg Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val				1306
405	410	415		
acg gtg ttc cag tac att ggg gag ctg tgc cga tac ctt gtc aac cag				1354

Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
 420 425 430

ccc ccg agc aag gca gaa cgt ggc cat aag gtc cgg ctg gca gtg ggc 1402
 Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
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agc ggg ctg cgc cca gat acc tgg gag cgt ttt gtg cgg cgc ttc ggg 1450
 Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
 450 455 460

ccc ctg cag gtg ctg gag aca tat gga ctg aca gag ggc aac gtg gcc 1498
 Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
 465 470 475 480

acc atc aac tac aca gga cag cgg ggc gct gtg ggg cgt gct tcc tgg 1546
 Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
 485 490 495

ctt tac aag cat atc ttc ccc ttc tcc ttg att cgc tat gat gtc acc 1594
 Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
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aca gga gag cca att cgg gac ccc cag ggg cac tgt atg gcc aca tct 1642
 Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
 515 520 525

cca ggt gag cca ggg ctg ctg gtg gcc ccg gta agc cag cag tcc cca 1690
 Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
 530 535 540

ttc ctg ggc tat gct ggc ggg cca gag ctg gcc cag ggg aag ttg cta 1738
 Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
 545 550 555 560

aag gat gtc ttc cgg cct ggg gat gtt ttc ttc aac act ggg gac ctg 1786
 Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
 565 570 575

ctg gtc tgc gat gac caa ggt ttt ctc cgc ttc cat gat cgt act gga 1834
 Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
 580 585 590

gac acc ttc agg tgg aag ggg gag aat gtg gcc aca acc gag gtg gca 1882
 Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
 595 600 605

gag gtc ttc gag gcc cta gat ttt ctt cag gag gtg aac gtc tat gga 1930
 Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
 610 615 620

gtc act gtg cca ggg cat gaa ggc agg gct gga atg gca gcc cta gtt 1978
 Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
 625 630 635 640

ctg cgt ccc ccc cac gct ttg gac ctt atg cag ctc tac acc cac gtg 2026
 Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
 645 650 655

tct gag aac ttg cca cct tat gcc cg^g ccc cga ttc ctc agg ctc cag 2074
 Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
 660 665 670

gag tct ttg gcc acc aca gag acc ttc aaa cag cag aaa gtt cg^g atg 2122
 Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
 675 680 685

gca aat gag ggc ttc gac ccc agc acc ctg tct gac cca ctg tac gtt 2170
 Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
 690 695 700

ctg gac cag gct gta ggt gcc tac ctg ccc ctc aca act gcc cg^g tac 2218
 Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
 705 710 715 720

agc gcc ctc ctg gca gga aac ctt cga atc tgagaacttc cacaccctgag 2268
 Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
 725 730

gcacccgtgaga gaggaactct gtgggggtggg ggccgttgca ggtgtactgg gctgtcaggg 2328
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 <212> PRT
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Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
 35 40 45

Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Pro Leu Leu Leu
 50 55 60

Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu
 65 70 75 80

Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg
 85 90 95

Ala Leu Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys
 100 105 110

Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His
 115 120 125

Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu
 130 135 140

Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp
 145 150 155 160

Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu
 165 170 175

Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Gly Ser Gly
 180 185 190

Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala
 195 200 205

Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly
 210 215 220

Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
 225 230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys
 245 250 255

Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu
 260 265 270

Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His
 275 280 285

Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu
 290 295 300

Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu
 305 310 315 320

Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser
 325 330 335

Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile
 340 345 350

Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp
 355 360 365

Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu
 370 375 380

Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser
 385 390 395 400

Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val
 405 410 415

Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
 420 425 430

Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
 435 440 445

Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
 450 455 460

Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
 465 470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
 485 490 495

Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
 500 505 510

Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
 515 520 525

Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
 530 535 540

Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
 545 550 555 560

Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
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Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
 580 585 590

Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
 595 600 605

Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
 610 615 620

Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
 625 630 635 640

Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
 645 650 655

Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
 660 665 670

Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
 675 680 685

Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
 690 695 700

Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
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Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
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<212> RNA

<213> Artificial Sequence

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Synthesized Oligo-cap Linker

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<213> Artificial Sequence

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<211> 21

<212> DNA

<213> Artificial Sequence

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
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<210> 7
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<210> 8
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<210> 9
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<212> DNA
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29

<210> 11

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<212> DNA

<213> Artificial Sequence

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aacagggctg cacgcgcctt

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<210> 12

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<212> DNA

<213> Artificial Sequence

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cgggatccca cctgcaacgg cccccacccc acagagttc

39